

FIGURE 1A

```

-185 GAATTCGGGGGGTTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAA
-125 CCCTCAACTGTCAACCCAGGCACTTGGGAGCTCTTGGACAGACCGAGTCCCGGGAAGCC
-65 CCAGCACTGCCGCTGCCACACTGCCCTGAGCCCCAAATGGGGGAGTGAGAGGCCATAGCTG
-28.
-30 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeu
-5 TCTGGCATGGGCCTCTCCACCGTGCCTGACCTGTGTGTCGCCGTGGTGTCTCTGGAGCTG
+1
-10 LeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGlu
55 TTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCTAGGGGACAGGGAG
***
10 LysArgAspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCys
115 AAGAGAGATAGTGTGTGTCCCCAAGGAAAATATATCCACCCTCAAAATAATTTCGATTTCG
30 CysThrLysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAsp
175 TGTACCAAGTGCCACAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGCAGGAT
50 ThrAspCysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHis
235 ACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCCACCTCAGACAC
70 CysLeuSerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThr
295 TGCCTCAGCTGTCCAAATGCCGAAAGGAAATGGGTGAGGTGAGATCTCTCTTTCGCACA
90 ValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlu
355 GTGGACCGGACACCGTGTGTGGCTGCAGGAAGAACCCAGTACCGGCATTATTGGAGTGAA

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FIGURE 1B

```

110 AsnLeuPheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCys
415 AACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTCAATGGGACCGTGACCTCTCTCG
130 GlnGluLysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlu
475 CAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTCTAAGAGAAAAACGAG
150 CysValSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln
535 TGTGTCCTCCTGTAGTAACGTAAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCGAG
170 IleGluAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIle
595 ATTGAGAAATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGTGGCCCTGGTTCATT
190 PhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArg
655 TTCTTTGGTCTTTTGCCCTTTTATCCCTCCTCTTCATTGGTTTAAATGATCGCTACCAACGG
210 TrpLysSerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGlu
715 TGGAAAGTCCAAGCTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGACGGGGAG
230 LeuGluGlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGly
775 CTTGAAGGAACACTACTAAGCCCTTGGCCCCCAACCCCAAGCTTCAGTCCCACTCCAGGC

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FIGURE 1C

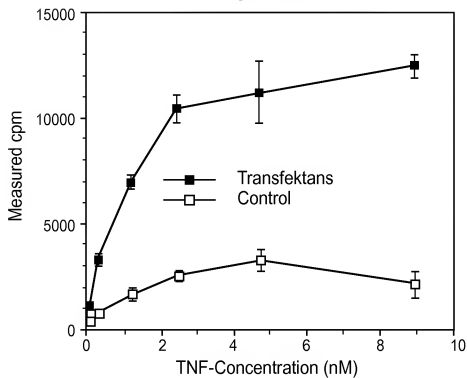
250 PheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThr  
835 TTCACCCCAACCTGGGCTTCAGTCCCGTGCCCGAGTTCACCTTCACCTCCAGCTCCACC  
270 TyrThrProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyr  
895 TATACCCCGGTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGGTGGCACCCCTAT  
290 GlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeu  
955 CAGGGGCTGACCCCATCCTTGCACAGCCCTCGCCCTCCGACCCCATCCCCAACCCCTT  
310 GlnLysTrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThr  
1015 CAGAAAGTGGAGGACAGCGGCCCAAGCCACAGAGCTAGACACTGATGACCCCGGACG  
330 LeuTyrAlaValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeu  
1075 CTGTACGCCGTGGTGGAGAACGTGCCCCCTTGGCTGGCTGGAAGGAATTCGTGGCGCCTA  
350 GlyLeuSerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGlu  
1135 GGGCTGAGCGACCAACGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAG  
370 AlaGlnTyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeu  
1195 GCGCAATACAGCATGCTGGCGACCTGGAGGGCGGCGACCGCGGCGGAGGCCACGCTG  
390 GluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGlu  
1255 GAGCTGCTGGGACCGCTGCTCCCGGACATGGACCTGCTGGGCTGCCTGGAGGACATCGAG

FIGURE 1D

410 GluAlaLeuCysGlyProAlaAlaLeuProAlaProAlaProSerLeuLeuArg  
 1315 GAGGCGCTTTGGGGCCCCCGCCCTCCCGCCGCGCCCACTTCTCAGATGAGGCTGC  
 1375 GCCCCTGGGGCAGCTCTAAGGACCGTCCCTGGGAGATCGCCTTCCAAACCCCACTTTTTC  
 1435 TGGAAAGGAGGGGTCCCTGCAGGGGCAAGCAGGAGCTAGCAGCCGCTACTTGGTGCTAAC  
 1495 CCCTCGATGTACATAGCTTTTCTCAGCTGCCTGGCGCGCCGACAGTCAGCGCTGTGCG  
 1555 CGCGGAGAGAGGTGCGCCGTGGGCTCAAGAGCCCTGAGTGGGTGTTTGCAGGATGAGGG  
 1615 ACGCTATGCCCTCATGCCCGTTTTTGGGTGTCTCACCAGCAAGGCTGCTCGGGGGCCCCCTG  
 1675 GTTCGTCCCTGAGCCTTTTTCAAGTGCATAAGCAGTTTTTTTGTGTTTGTGTTTT  
 1735 GTTTTGTGTTTTTAAATCAATCATGTTACACTAATAGAAACTTGGCACTCCTGTGCCCTCTG  
 1795 CCTGGACAAGCACATAGCAAGCTGAACCTGCTTAAGGCAGGGGCGAGCACGGAACAATGG  
 1855 GGCCTTCAGCTGGAGCTGTGGACTTTTGTACATACACTAAAAATTCTGAAAGTTAAAAAAA  
 1915 AACCCGAATTC

# REPLACEMENT SHEET

## Figure 2A



## Figure 2B

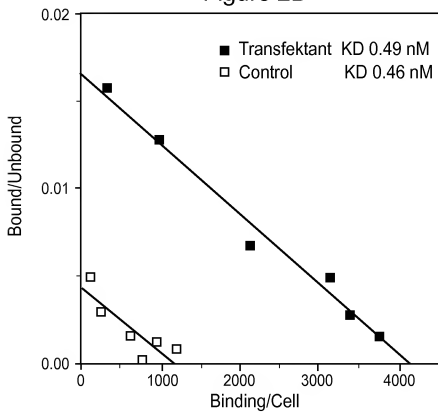


Figure 3

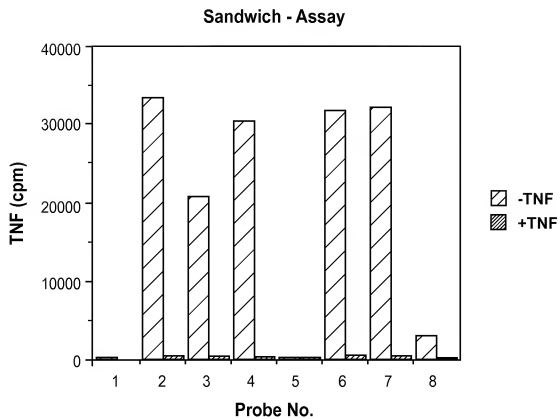


FIGURE 4A

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1 SerAspSerValCysAspSerCysGluAspSerThrTyrThrGlnLeuTrpAsnTrpVal
1 TCGGACTCCGTGTGTGACTCCTGTGAGGACAGCACATACACCCAGCTCTGGAACTGGGTT
.
.
21 ProGluCysLeuSerCysGlySerArgCysSerSerAspGlnValGluThrGlnAlaCys
61 CCCGAGTGTGAGCTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACACTCAAGCCTGC
.
.
41 ThrArgGluGlnAsnArgIleCysThrCysArgProGlyTrpTyrCysAlaLeuSerLys
121 ACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCGCGCTGAGCAAG
.
.
61 GlnGluGlyCysArgLeuCysAlaProLeuProLysCysArgProGlyPheGlyValAla
181 CAGGAGGGGTGCCGGCTGTGCGCGCGCTGCCGAAGTGCCGCCCGGGCTTCGGCGTGGCC
.
.
81 ArgProGlyThrGluThrSerAspValValCysLysProCysAlaProGlyThrPheSer
241 AGACCAGGAACCTGAAACATCAGACGTGGTGTGCAAGCCCTGTGCCCGGGGACGTTCTCC
.
.
101 AsnThrThrSerSerThrAspIleCysArgProHisGlnIleCysAsnValValAlaIle
301 AACACGACTTCATCCACGGATATTTCAGGCCCCCACCAGATCTGTAACGTGGTGGCCATC
.
.
121 ProGlyAsnAlaSerArgAspAlaValCysThrSerThrSerProThrArgSerMetAla
361 CCTGGGAATGCAAGCAGGGATGCAGTCTGCACGTCCACGTCCCCCACCAGGAGTATGGCC
.
.
141 ProGlyAlaValHisLeuProGlnProValSerThrArgSerGlnHisThrGlnProSer
421 CCAGGGGCAGTACACTTACCCAGCCAGTGTCCACACGATCCCAACACACGACGCCAAGT

```

FIGURE 4B

161 ProGluProSerThrAlaProSerThrSerPheLeuLeuProMetGlyProSerProPro  
 481 CCAGAACCCAGCACTGCTCCAAGCACCTCCTTCTCTGCTCCCAATGGGCCCCAGCCCCC  
 181 AlaGluGlySerThrGlyAspPheAlaLeuProValGlyLeuIleValGlyValThrAla  
 541 GCTGAAGGGAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGACAGCC  
 201 LeuGlyLeuLeuIleIleGlyValValAsnCysValIleMetThrGlnValLysLys  
 601 TTGGGTCTACTAATAATAGGAGTGGTGAACCTGTGTTCATCATGACCCAGGTGAAAAAGAAG  
 221 ProLeuCysLeuGlnArgGluAlaLysValProHisLeuProAlaAspLysAlaArgGly  
 661 CCCTTGTGCCTGCAGAGAGAGCAAGCAAGGTGCCTCACTTGCCTGCCGATAAGGCCCGGGGT  
 241 ThrGlnGlyProGluGlnGlnHisLeuLeuIleThrAlaProSerSerSerSerSer  
 721 ACACAGGGCCCCGAGCAGCAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCC  
 261 LeuGluSerSerAlaSerAlaLeuAspArgAlaProThrArgAsnGlnProGlnAla  
 781 CTGGAGAGCTCGGCCAGTGCCTTGGACAGAGGGGGCCCCACTCGGAACCCAGCCACAGGCA  
 281 ProGlyValGluAlaSerGlyAlaGlyGluAlaArgAlaSerThrGlySerSerAlaAsp  
 841 CCAGGCGTGGAGGCCAGTGGGGCCGGGAGGCCCGGGCCAGCACCCGGGAGCTCAGCAGAT  
 301 SerSerProGlyGlyHisGlyThrGlnValAsnValThrCysIleValAsnValCysSer  
 901 TCTTCCCCTGGTGGCCATGGGACCCAGGTCAATGTCACTGATCGTGAACGCTCTGTAGC



FIGURE 4D

1921 GCCGGGCGTGGTGGCGGGCACCTATAGTCCCAGCTACTCAGAAGCCTGAGGCTGGGAAAT  
1981 CGTTTGAAACCCGGGAAGCGGAGGTTCAGGGAGCCGAGATCAGGCCACTGCACTCCAGCC  
2041 TGGCGGACAGAGCGAGAGTCTGTCTCAAAAGAAAAAAGCACCGCCTCCAAATGCT  
2101 AACTTGTCTTTTGTACCATGGTGTGAAAGTCAGATGCCCCAGAGGGCCCCAGGCAGGCCAC  
2161 CATATTCAGTGCTGTGGCCTGGGCAAGATAACGCACCTTCTAACTAGAAATCTGCCAATTT  
2221 TTTAAAAAAGTAAGTACCACCTCAGGCCAACAAAGCCAAAGCCAAACTCTGCCAGC  
2281 CACATCCAACCCCCACCTGCCATTTCACACCTCCGCCTTCACTCCGGTGTGCCTGCAG

# REPLACEMENT SHEET

1 MAPVAVWAAL AVGLELWAAA HALPAQVAFT PYAFEPGSTC RLREYYDQTA  
 51 QMCCSKCSPG QNAKVFC<sup>+</sup>TKT SDTVCDSCED STYTQLWNWV PECLSCGSR<sup>+</sup>C  
 101 SSDQVETQAC TREQNRICT<sup>+</sup>C R<sup>+</sup>PGWYCALSK QEGCRLCAPL R<sup>+</sup>KCRPGFGVA  
 151 R<sup>+</sup>PGTETSDVV CKPCAPGTFS NTTSSTDICR PHQICNVVAI PGNASMDAVC<sup>+</sup>  
 201 TSTSPTSRMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS FLLPMGPSPP  
 251 AEGSTGDFAL PVGLIVGVTA LGLLIIGVVN CVINTQVKKK PLC<sup>+</sup>LQREAKV  
 301 PHLPADKARG TQGPEQQHLL ITAPSSSSSS LESSASALDR RAPTRNQFQA  
 351 PGVEASGAGE ARASTGSSDS SPGGHGTQVN VTCIVNVCSS SDHSSQC<sup>+</sup>SSQ  
 401 ASSTMGDTDS SPSESPEDEQ VPFSKEECA<sup>+</sup>F RSQLETPETL LGSTEEKPLP  
 451 LGVPDAGMKP S

FIGURE 5

FIGURE 6A

1 S D T V C D S C E D S T Y T Q L W N W V  
 1 tcggacacgtgtgactcctgtgaggacagcacatacacccagctctggaactgggtt  
 1 10 20 30 40 50  
 21 P E C L S C G S R C S S D Q V E T Q A C  
 61 ccgagtgctgagctgtggctcccgctgtagctctgaccaggtggaactcaagcctgc  
 61 70 80 90 100 110  
 41 T R E Q N R I C T C R P G W Y C A L S K  
 121 actcgggaacagacgcacatctgcacctgcaggcccggtggtactgcgcgtgagcaag  
 121 130 140 150 160 170  
 61 Q E G C R L C A P L P K C R P G F G V A  
 181 caggagggtgccggctgtgcgcgcgctgcccgaagtgccgcccggcttcggcgtggcc  
 181 190 200 210 220 230  
 81 R P G T E T S D V V C K P C A P G T F S  
 241 agaccaggaactgaaacatcagacgtggtgtgcaagccctgtgccccgggacgttctcc  
 241 250 260 270 280 290  
 101 N T T S S T D I C R P H Q I C N V V A I  
 301 aacacgacttcacaggatatttgaggccccaccagatctgtaacgtggtggccatc  
 301 310 320 330 340 350

FIGURE 6B

121 P G N A S R D A V C T S T S P T R S M A  
 361 cctgggaatgcaagcaggatgcagtctgcacgtccacgtccccacccggagtatggcc  
 361 370 380 390 400 410  
 141 P G A V H L P Q P V S T R S Q H T Q P S  
 421 ccaggggcagtagacattacccagcagtcacacgattcccaacacagcagccaagt  
 421 430 440 450 460 470  
 161 P E P S T A P S T S F L L P M G P S P P  
 481 ccagaaccagcactgctccaagcacctccttctcgtcccaatgggccccagccccc  
 481 490 500 510 520 530  
 181 A E G S T G D F A L P V G L I V G V T A  
 541 gctgaaggaggcactggcgacttcgctcttccagttggactgattgtgggtgtgacagcc  
 541 550 560 570 580 590  
 201 L G L L I I G V V N C V I M T Q V K K K  
 601 ttgggtctactaataataggagtggagaactgtgtcatcatgacccaggtgaaaaaag  
 601 610 620 630 640 650  
 221 P L C L Q R E A K V P H L P A D K A R G  
 661 cccttgctgcctgcagagagaagccaaggtgcctcacttgcctgccgataaggccggggt  
 661 670 680 690 700 710

FIGURE 6C

241 T Q G P E Q Q H L L I T A P S S S S S  
721 acacagggcccgagcagcagcacctgctgatcacagcgccgagctccagcagcagctcc  
721 730 740 750 760 770

261 L E S S A S A L D R R A P T R N Q P Q A  
781 ctggagagctcgccagtcgcttgacagaaggcgccactcggaaccagccacaggca  
781 790 800 810 820 830

281 P G V E A S G A G E A R A S T G S S A D  
841 ccaggcgtggaggccagtggggcccgggagggccagcacccgggagctcagcagat  
841 850 860 870 880 890

301 S S P G G H G T Q V N V T C I V N V C S  
901 tcttcccctggcggccatgggaccagggtcaatgtcacctgcacgtgaacgtctgtagc  
901 910 920 930 940 950

321 S S D H S S Q C S S Q A S S T M G D T D  
961 agctctgaccacagctcacagtgctctccccaagccagctccacaatgggagacacagat  
961 970 980 990 1000 1010

341 S S P S E S P K D E Q V P F S K E E C A  
1021 tccagcccctcgaggtccccgaaggacgagcaggtcccccttctccaaggaggaatgtgcc  
1021 1030 1040 1050 1060 1070



FIGURE 6E

1681 agactgcgggatggtcctctgggctctgtgcaggaggaggtggcagccctgtagggaacg  
 1681 1690 1700 1710 1720 1730  
 1741 gggtccttcaagttagctcaggaggcttggaaagcatcacctcagggcaggtgcagtggc  
 1741 1750 1760 1770 1780 1790  
 1801 tcacgcctatgatcccagcactttgggaggctgagcggtggatcacctcaggttagga  
 1801 1810 1820 1830 1840 1850  
 1861 gttcgagaccagcctggccaacatggtaaaaccccatctctactaaaaatacagaaatta  
 1861 1870 1880 1890 1900 1910  
 1921 gccgggctggtggcggcacctatagtcacagctactcagaagcctgaggctgggaaat  
 1921 1930 1940 1950 1960 1970  
 1981 cgtttgaacccgggaagcggaggttgaggagccgagatcacgccactgcactccagcc  
 1981 1990 2000 2010 2020 2030  
 2041 tggggcacagagcgagagtgctgtctcaaaagaaaaaaagcaccgcctccaaatgct  
 2041 2050 2060 2070 2080 2090  
 2101 aacttgctcctttgtaccatggtgtgaaagtccagatgccagagggcccgagggccac  
 2101 2110 2120 2130 2140 2150  
 2161 catattcagtgctgtggcctggcgaagataacgcacttctaactagaaatctgccaat  
 2161 2170 2180 2190 2200 2210  
 2221 tttaaaaaagtaagtaccactcagggcacaagccaaagcacaagccaaactctgccagc  
 2221 2230 2240 2250 2260 2270  
 2281 cacatccaaacccccacactgccatttgacccctccgccttcactccggtgtgcctgcag  
 2281 2290 2300 2310 2320 2330